

mertz 308-4229

CRF Error Corrected by the STIC Systems Branch

CRF Processing Date: 2/13/98  
Edited by: [Signature]  
Verified by: [Signature] (STIC staff)

Serial Number: 08/910,733

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☒ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/910,733DATE: 02/13/98  
TIME: 10:58:50

INPUT SET: S23457.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

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SEQUENCE LISTINGDoes Not Comply  
Corrected Diskette Needed

## (1) General Information:

(i) APPLICANT: COLOTTA, Francesco  
MUZIO, Marta  
MANTOVANI, Alberto(ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,  
AND ANTIBODIES THERETO

(iii) NUMBER OF SEQUENCES: 17

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BROWDY AND NEIMARK  
(B) STREET: 419 Seventh Street, N.W., Suite 300  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20004

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

insert header

&gt; (vi) CURR APP DATA:

## (vii) (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/476,860  
(B) FILING DATE: 07-JUN-1995

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IT MI 94 A 002097  
(B) FILING DATE: 13-OCT-1994

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: YUN, Allen C.  
(B) REGISTRATION NUMBER: 37,971  
(C) REFERENCE/DOCKET NUMBER: COLOTTA=1A

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-628-5197  
(B) TELEFAX: 202-737-3528

## (2) INFORMATION FOR SEQ ID NO: 1:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/910,733DATE: 02/13/98  
TIME: 10:58:53

INPUT SET: S23457.raw

47  
48 (i) SEQUENCE CHARACTERISTICS:  
49 (A) LENGTH: 25 base pairs  
50 (B) TYPE: nucleic acid  
51 (C) STRANDEDNESS: single  
52 (D) TOPOLOGY: linear  
53  
54 (ii) MOLECULE TYPE: DNA  
55  
56 (iii) HYPOTHETICAL: NO  
57  
58 (ix) FEATURE:  
59 (D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5  
60  
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
62  
63 CTGACTTGTA TGAAGAAGGA GGTGG 25  
64  
65 (2) INFORMATION FOR SEQ ID NO: 2:  
66  
67 (i) SEQUENCE CHARACTERISTICS:  
68 (A) LENGTH: 20 base pairs  
69 (B) TYPE: nucleic acid  
70 (C) STRANDEDNESS: single  
71 (D) TOPOLOGY: linear  
72  
73 (ii) MOLECULE TYPE: DNA  
74  
75 (iii) HYPOTHETICAL: NO  
76  
77 (ix) FEATURE:  
78 (D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding  
79 to 60-79 of B-actin  
80  
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
82  
83 GCGCTCGTCG TCGACAACGG 20  
84  
85 (2) INFORMATION FOR SEQ ID NO: 3:  
86  
87 (i) SEQUENCE CHARACTERISTICS:  
88 (A) LENGTH: 21 base pairs  
89 (B) TYPE: nucleic acid  
90 (C) STRANDEDNESS: single  
91 (D) TOPOLOGY: linear  
92  
93 (ii) MOLECULE TYPE: DNA  
94  
95 (iii) HYPOTHETICAL: NO  
96  
97 (ix) FEATURE:  
98 (D) OTHER INFORMATION: RT-PCR backward oligonucleotide  
99 complementary to 430-449

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/910,733DATE: 02/13/98  
TIME: 10:58:57

INPUT SET: S23457.raw

100  
101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
102  
103 GATAGACAAC GTACATGGCT G 21  
104  
105 (2) INFORMATION FOR SEQ ID NO: 4:  
106  
107 (i) SEQUENCE CHARACTERISTICS:  
108 (A) LENGTH: 87 base pairs  
109 (B) TYPE: nucleic acid  
110 (C) STRANDEDNESS: single  
111 (D) TOPOLOGY: linear  
112  
113 (ii) MOLECULE TYPE: DNA  
114  
115 (iii) HYPOTHETICAL: NO  
116  
117 (ix) FEATURE:  
118 (D) OTHER INFORMATION: Sequence of sIL-lra not in common  
119  
120 (ix) FEATURE:  
121 (A) NAME/KEY: CDS  
122 (B) LOCATION: 24..86  
123  
124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
125  
126 GAATTCGGG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT 50  
127 Met Glu Ile Cys Arg Gly Leu Arg Ser  
128 1 5  
129  
130 CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G 87  
131 His Leu Ile Thr Leu Leu Leu Phe Leu Phe His Ser  
132 10 15 20  
133  
134  
135 (2) INFORMATION FOR SEQ ID NO: 5:  
136  
137 (i) SEQUENCE CHARACTERISTICS:  
138 (A) LENGTH: 21 amino acids  
139 (B) TYPE: amino acid  
140 (D) TOPOLOGY: linear  
141  
142 (ii) MOLECULE TYPE: protein  
143  
144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
145  
146 Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu  
147 1 5 10 15  
148  
149 Phe Leu Phe His Ser  
150 20  
151  
152 (2) INFORMATION FOR SEQ ID NO: 6:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/910,733DATE: 02/13/98  
TIME: 10:59:00

INPUT SET: S23457.raw

153  
154 (i) SEQUENCE CHARACTERISTICS:  
155 (A) LENGTH: 42 base pairs  
156 (B) TYPE: nucleic acid  
157 (C) STRANDEDNESS: single  
158 (D) TOPOLOGY: linear  
159  
160 (ii) MOLECULE TYPE: DNA  
161  
162 (iii) HYPOTHETICAL: NO  
163  
164 (ix) FEATURE:  
165 (D) OTHER INFORMATION: Sequence of intracellular IL-1ra  
166 typeI not in common  
167  
168 (ix) FEATURE:  
169 (A) NAME/KEY: CDS  
170 (B) LOCATION: 33..41  
171  
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
173  
174 CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA G 42  
175 Met Ala Leu  
176 1  
177  
178  
179 (2) INFORMATION FOR SEQ ID NO: 7:  
180  
181 (i) SEQUENCE CHARACTERISTICS:  
182 (A) LENGTH: 105 base pairs  
183 (B) TYPE: nucleic acid  
184 (C) STRANDEDNESS: single  
185 (D) TOPOLOGY: linear  
186  
187 (ii) MOLECULE TYPE: DNA  
188  
189 (iii) HYPOTHETICAL: NO  
190  
191 (ix) FEATURE:  
192 (D) OTHER INFORMATION: Sequence of intracellular IL-1ra  
193 typeII not in common  
194  
195 (ix) FEATURE:  
196 (A) NAME/KEY: CDS  
197 (B) LOCATION: 33..104  
198  
199 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
200  
201  
202 CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA GCT GAC TTG TAT 53  
203 Met Ala Leu Ala Asp Leu Tyr  
204 1 5  
205

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/910,733

DATE: 02/13/98

TIME: 10:59:04

INPUT SET: S23457.raw

206 GAA GAA GGA GGT GGA GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA 101  
 207 Glu Glu Gly Gly Gly Gly Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser  
 208 10 15 20

209  
 210 AAG G 105  
 211 Lys  
 212  
 213

## (2) INFORMATION FOR SEQ ID NO: 8:

215  
 216 (i) SEQUENCE CHARACTERISTICS:  
 217 (A) LENGTH: 24 amino acids  
 218 (B) TYPE: amino acid  
 219 (D) TOPOLOGY: linear  
 220

221 (ii) MOLECULE TYPE: protein  
 222

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

223  
 224  
 225 Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu  
 226 1 5 10 15  
 227  
 228 Gly Glu Asp Asn Ala Asp Ser Lys  
 229 20  
 230

## (2) INFORMATION FOR SEQ ID NO: 9:

231  
 232  
 233 (i) SEQUENCE CHARACTERISTICS:  
 234 (A) LENGTH: 474 base pairs  
 235 (B) TYPE: nucleic acid  
 236 (C) STRANDEDNESS: single  
 237 (D) TOPOLOGY: linear  
 238

239 (ii) MOLECULE TYPE: DNA  
 240

241 (iii) HYPOTHETICAL: NO  
 242

## (ix) FEATURE:

243  
 244 (D) OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G  
 245 was added in the first position, for computer program  
 246 reason, in order to encode the first amino acid Glu  
 247 and further in order to avoid the creation of a stop  
 248 codon in the inner region of the sequence  
 249

## (ix) FEATURE:

250  
 251 (A) NAME/KEY: CDS  
 252 (B) LOCATION: 1..468  
 253

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

254  
 255  
 256 GAG ACG ATC TGC CGA CCC TCT GGG AGA AAA TCC AGC AAG ATG CAA GCC 48  
 257 Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala  
 258 1 5 10 15

PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/08/910,733**

DATE: 02/13/98  
TIME: 10:59:08

*INPUT SET: S23457.raw*

APPLICATION NUMBER  
FILING DATE  
CLASSIFICATION  
CURRENT APPLICATION DATA